



1007P1D1seq1 (new)-response to 6-29-04 action.txt
Patin Docke

Sequence Listing

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ashkenazi, Avi J.
- (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genentech, Inc.
 - (B) STREET: 1 DNA Way
 - (C) CITY: South San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US/09/993,234A
 - (B) FILING DATE: 19-NOV-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/828683
 - (B) FILING DATE: 31-MAR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/625328
 - (B) FILING DATE: 1-Apr-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/710802
 - (B) FILING DATE: 23-Sep-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Marschang, Diane L.
 - (B) REGISTRATION NUMBER: 35,600
 - (C) REFERENCE/DOCKET NUMBER: P1007P1D1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650/225-5416
 - (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5					10					15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
			20						25					30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
			35						40					45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
			50						55					60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
			65						70					75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
			80						85					90
Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu
			95						100					105
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly
			110						115					120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro
			125						130					135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His
			140						145					150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys
			155						160					165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro
			170						175					180

Thr

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 433 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50

TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCCTGC ACGGAGCCCT GCGCAACTCC 150

ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200

TAATTCTGAA TGTGCCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250

TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300

CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350

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CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1438 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCC GCCTCC 250
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
AGATTGGTCT GTTTTGTTCG AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550

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GCCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600
 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCGCT 650
 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
 GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATT 1150
 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
 ACCTATTAAT TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 417 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu
1				5				10						15
Leu	Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser
			20					25						30
Pro	Arg	Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu
			35					40						45
Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro
			50					55						60
Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln
			65					70						75
Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala
			80					85						90

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Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu
				95					100					105
Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly
				110					115					120
Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	Ser	Pro
				125					130					135
Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	His
				140					145					150
Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys
				155					160					165
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro
				170					175					180
Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys
				185					190					195
Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu
				200					205					210
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg
				215					220					225
His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly
				230					235					240
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu
				245					250					255
Asp	Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys
				260					265					270
Ile	Cys	Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr
				275					280					285
Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp
				290					295					300
Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr
				305					310					315
Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln
				320					325					330
Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	Val	Pro	Ala	Arg
				335					340					345
Arg	Trp	Lys	Glu	Phe	Val	Arg	Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu
				350					355					360
Ile	Glu	Ala	Val	Glu	Val	Glu	Ile	Gly	Arg	Phe	Arg	Asp	Gln	Gln
				365					370					375
Tyr	Glu	Met	Leu	Lys	Arg	Trp	Arg	Gln	Gln	Gln	Pro	Ala	Gly	Leu
				380					385					390
Gly	Ala	Val	Tyr	Ala	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gly	Cys
				395					400					405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1634 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCGTC GGAGGGCT ATG GAG 94
 Met Glu
 1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
 Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
 5 10 15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
 20 25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
 30 35 40

AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
 45 50

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CAC	TAC	CTG	AAG	GCC	CCT	TGC	ACG	GAG	CCC	TGC	GGC	AAC	289
His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	Cys	Gly	Asn	
55					60					65			
TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	328
Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
		70					75					80	
TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	367
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	
				85					90				
GCC	TGT	GAT	GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	406
Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	
	95					100					105		
TGT	TCA	GCA	GTG	GCC	GAC	ACC	CGC	TGT	GGC	TGT	AAG	CCA	445
Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	Lys	Pro	
			110					115					
GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	CAA	TGT	GTC	AGC	484
Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	
120					125					130			
AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	GGG	523
Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	
		135					140					145	
GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	562
Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	
				150					155				
GAT	ACT	GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	601
Asp	Thr	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	
	160					165					170		
CAT	GGC	GAT	GGC	TGC	GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	640
His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	
			175					180					
GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	GCT	GTC	TGT	GGC	TGG	679
Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	
185					190					195			
AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	GGC	CTT	718
Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	
		200					205					210	
GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	757
Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	
				215					220				
TAC	CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	796
Tyr	Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	
	225					230					235		
GAT	GAA	GCT	GGG	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	835
Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	
			240					245					
ACC	CAT	CTG	TCA	CCC	TTG	GAC	AGC	GCC	CAC	ACC	CTT	CTA	874
Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	Leu	
250					255					260			

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GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913
Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln
265 270 275

TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952
Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
280 285

CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
290 295 300

CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro
305 310

ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
315 320 325

ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108
Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp
330 335 340

GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
Ala Val Pro Ala Arg Trp Lys Glu Phe Val Arg Thr
345 350

CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186
Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val
355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
370 375

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

(2) INFORMATION FOR SEQ ID NO:10:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile
1				5					10					15
Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys
				20					25					30
Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser	Gly
				35					40					45
Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys
				50					55					60
Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys
				65					70					75
Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr
				80					85					90
Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser
				95					100					105
Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln
				110					115					120
Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn
				125					130					135
Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr
				140					145					150

Lys Leu Cys Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

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Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys
 1           5           10           15
Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr
          20           25           30
Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr
          35           40           45
Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser
          50           55           60
Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu
          65           70           75
Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
          80           85           90
Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys
          95          100          105
Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp
          110          115          120
Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr
          125          130          135
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val
          140          145          150
Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala Val Cys Thr
          155          160
    
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(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Thr Cys Arg Asp Gln Glu Lys Glu Tyr Tyr Glu Pro Gln His Arg
 1           5           10           15
Ile Cys Cys Ser Arg Cys Pro Pro Gly Thr Tyr Val Ser Ala Lys
          20           25           30
Cys Ser Arg Ile Arg Asp Thr Val Cys Ala Thr Cys Ala Glu Asn
          35           40           45
    
```

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

```

Ser Tyr Asn Glu His Trp Asn Tyr Leu Thr Ile Cys Gln Leu Cys
      50                      55                      60
Arg Pro Cys Asp Pro Val Met Gly Leu Glu Glu Ile Ala Pro Cys
      65                      70                      75
Thr Ser Lys Arg Lys Thr Gln Cys Arg Cys Gln Pro Gly Met Phe
      80                      85                      90
Cys Ala Ala Trp Ala Leu Glu Cys Thr His Cys Glu Leu Leu Ser
      95                      100                     105
Asp Cys Pro Pro Gly Thr Glu Ala Glu Leu Lys Asp Glu Val Gly
      110                     115                     120
Lys Gly Asn Asn His Cys Val Pro Cys Lys Ala Gly His Phe Gln
      125                     130                     135
Asn Thr Ser Ser Pro Ser Ala Arg Cys Gln Pro His Thr Arg Cys
      140                     145                     150
Glu Asn Gln Gly Leu Val Glu Ala Ala Pro Gly Thr Ala Gln Ser
      155                     160                     165
Asp Thr Thr Cys Lys
      170

```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro
  1      5      10
Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly
      20      25      30
Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr
      35      40      45
Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys
      50      55      60
Asp Glu Gly His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr
      65      70      75
Gln Asn Thr Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser
      80      85      90
Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly
      95     100     105
Ile Ile Lys Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys
      110     115

```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

(A) LENGTH: 159 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys
 1           5           10           15
Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
          20           25           30
Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp
          35           40           45
Val Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val
          50           55           60
Gly Leu Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala
          65           70           75
Val Cys Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly
          80           85           90
Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val
          95          100          105
Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro
          110          115          120
Asp Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu
          125          130          135
Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys
          140          145          150
Thr Arg Trp Ala Asp Ala Glu Cys Glu
          155
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser
 1           5           10           15
Leu Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe
          20           25           30
Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp
          35           40           45
Thr Trp Asn Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp
          50           55           60
Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr
          65           70           75
```

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Asp	Thr	Ile	Cys	Thr	Cys	Glu	Glu	Gly	Trp	His	Cys	Thr	Ser	Glu
				80					85					90
Ala	Cys	Glu	Ser	Cys	Val	Leu	His	Arg	Ser	Cys	Ser	Pro	Gly	Phe
				95					100					105
Gly	Val	Lys	Gln	Ile	Ala	Thr	Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu
				110					115					120
Pro	Cys	Pro	Val	Gly	Phe	Phe	Ser	Asn	Val	Ser	Ser	Ala	Phe	Glu
				125					130					135
Lys	Cys	His	Pro	Trp	Thr	Ser	Cys	Glu	Thr	Lys	Asp	Leu	Val	Val
				140					145					150
Gln	Gln	Ala	Gly	Thr	Asn	Lys	Thr	Asp	Val	Val	Cys	Gly		
				155					160					

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ser	Cys	Pro	Glu	Arg	His	Tyr	Trp	Ala	Gln	Gly	Lys	Leu	Cys	Cys
1				5					10					15
Gln	Met	Cys	Glu	Pro	Gly	Thr	Phe	Leu	Val	Lys	Asp	Cys	Asp	Gln
				20					25					30
His	Arg	Lys	Ala	Ala	Gln	Cys	Asp	Pro	Cys	Ile	Pro	Gly	Val	Ser
				35					40					45
Phe	Ser	Pro	Asp	His	His	Thr	Arg	Pro	His	Cys	Glu	Ser	Cys	Arg
				50					55					60
His	Cys	Asn	Ser	Gly	Leu	Leu	Val	Arg	Asn	Cys	Thr	Ile	Thr	Ala
				65					70					75
Asn	Ala	Glu	Cys	Ala	Cys	Arg	Asn	Gly	Trp	Gln	Cys	Arg	Asp	Lys
				80					85					90
Glu	Cys	Thr	Glu	Cys	Asp	Pro	Leu	Pro	Asn	Pro	Ser	Leu	Thr	Ala
				95					100					105
Arg	Ser	Ser	Gln	Ala	Leu	Ser	Pro	His	Pro	Gln	Pro	Thr	His	Leu
				110					115					120

Pro

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

```

Thr Cys His Gly Asn Pro Ser His Tyr Tyr Asp Lys Ala Val Arg
 1      5      10      15
Arg Cys Cys Tyr Arg Cys Pro Met Gly Leu Phe Pro Thr Gln Gln
 20      25      30
Cys Pro Gln Arg Pro Thr Asp Cys Arg Lys Gln Cys Glu Pro Asp
 35      40      45
Tyr Tyr Leu Asp Glu Ala Asp Arg Cys Thr Ala Cys Val Thr Cys
 50      55      60
Ser Arg Asp Asp Leu Val Glu Lys Thr Pro Cys Ala Trp Asn Ser
 65      70      75
Ser Arg Val Cys Glu Cys Arg Pro Gly Met Phe Cys Ser Thr Ser
 80      85      90
Ala Val Asn Ser Cys Ala Arg Cys Phe Phe His Ser Val Cys Pro
 95      100     105
Ala Gly Met Ile Val Lys Phe Pro Gly Thr Ala Gln Lys Asn Thr
 110     115     120
Val Cys Glu

```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

His Cys Val Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His
 1      5      10      15
Glu Cys Arg Pro Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser
 20      25      30
Gln Asn Thr Val Cys Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp
 35      40      45
Val Val Ser Ser Lys Pro Cys Lys Pro Cys Thr Trp Cys Asn Leu
 50      55      60
Arg Ser Gly Ser Glu Arg Lys Gln Leu Cys Thr Ala Thr Gln Asp
 65      70      75
Thr Val Cys Arg Cys Arg Ala Gly Thr Gln Pro Leu Asp Ser Tyr
 80      85      90
Lys Pro Gly Val Asp Cys Ala Pro Cys Pro Pro Gly His Phe Ser
 95      100     105
Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys Thr Leu
 110     115     120
Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn Ser Ser Asp Ala
 125     130     135

```

Ile Cys Glu

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
 1           5           10           15
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
          20           25           30
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
          35           40           45
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
          50           55           60
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
          65           70           75
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
          80           85           90
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
          95          100          105
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
          110          115          120
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
          125          130          135
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
          140          145          150
Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
          155          160          165
Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
          170          175          180
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
          185          190          195
Leu Pro
    
```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	1	5	10	15
Ala	Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	20	25	30	
Asn	Ser	Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	35	40	45	
Thr	Gln	Asn	Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	50	55	60	
Lys	Pro	Cys	Pro	Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	65	70	75	
Asn	Gly	Asp	Glu	Pro	Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	80	85	90	
Tyr	Thr	Asp	Lys	Ala	His	Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	95	100	105	
Leu	Cys	Asp	Glu	Gly	His	Gly	Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	110	115	120	
Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg	Cys	Lys	Pro	Asn	Phe	Phe	Cys	125	130	135	
Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp	Pro	Cys	Thr	Lys	Cys	Glu	140	145	150	
His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr	Ser	Asn	Thr	Lys	Cys	155	160	165	

Lys Glu

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	1	5	10	15
Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln	20	25	30	
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	35	40	45	
Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	50	55	60	
Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	65	70	75	

Ile Glu Glu

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg
 1           5           10
Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp
                20           25           30
Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn
                35           40           45
Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile
                50           55           60
Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
                65           70           75
Gln Thr
```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Ile Cys Asp Asn Val Gly Lys Asp Trp Arg Arg Leu Ala Arg Gln
 1           5           10           15
Leu Lys Val Ser Asp Thr Lys Ile Asp Ser Ile Glu Asp Arg Tyr
                20           25           30
Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser Leu Arg Ile Trp
                35           40           45
Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His Leu Val Gly
                50           55           60
Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu Val
                65           70
```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Asn Arg Pro Leu Ser Leu Lys Asp Gln Gln Thr Phe Ala Arg Ser
 1           5           10           15
```

P1007P1D1seq1 (new)-response to 6-29-04 action.txt

```

Val Gly Leu Lys Trp Arg Lys Val Gly Arg Ser Leu Gln Arg Gly
    20                25                30
Cys Arg Ala Leu Arg Asp Pro Ala Leu Asp Ser Leu Ala Tyr Glu
    35                40                45
Tyr Glu Arg Glu Gly Leu Tyr Glu Gln Ala Phe Gln Leu Leu Arg
    50                55                60
Arg Phe Val Gln Ala Glu Gly Arg Arg Ala Thr Leu Gln Arg Leu
    65                70                75
Val Glu

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Ile Arg Glu Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys
  1          5          10          15
Leu Gly Phe Thr Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr
    20          25          30
Glu Arg Asp Gly Leu Lys Glu Lys Val Tyr Gln Met Leu Gln Lys
    35          40          45
Trp Val Met Arg Glu Gly Ile Lys Gly Ala Thr Val Gly Lys Leu
    50          55          60
Ala Gln Ala Leu His Gln Cys Ser Arg Ile Asp Leu Leu Ser Ser
    65          70          75
Leu Thr

```

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Ala Val Ala Phe Tyr Ile Pro Asp Gln Ala Thr Leu Leu Arg
  1          5          10          15
Glu Ala Glu Gln Lys Glu Gln Gln Ile Leu Arg Leu Arg Glu Ser
    20          25          30
Gln Trp Arg Phe Leu Ala Thr Val Val Leu Glu Thr Leu Lys Gln
    35          40          45
Tyr Thr Ser Cys His Pro Lys Thr Gly Arg Lys Ser Gly Lys Tyr
    50          55          60

```

Arg Lys Pro P1007P1D1seq1 (new)-response to 6-29-04 action.txt